

Genetic profile for Quinault NFH

Fall chum salmon

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National Fish Hatchery Broodstock Genetic Profile

Facility:	Quinault National Fish Hatchery
Stock:	Fall chum salmon (<i>Oncorhynchus keta</i>)
Parental stock:	Founded with local stocks from the Quinault River. Received occasional egg imports from other Washington stocks, especially from Walcott Slough (Hood Canal). Out-of-basin egg imports ended in 1985.
Year founded:	Began in 1969.
Generation time:	
Segregation/Integration history:	Segregated. However, individuals are not marked to distinguish them from natural-origin adults returning to the Quinault River. Some natural spawning occurs below the hatchery weir and natural-origin adults are not segregated should they reach the hatchery.

Table 1: Broodstock samples analyzed:

Description	Year	<i>n</i>	Life stage	Data source	Code
Quianult NFH	2001	95	Returning adult	ADFG	QUIN01F
Quianult NFH	2008	95	Returning adult	ADFG	QUIN01F
Quianult NFH	2010	95	Returning adult	ADFG	QUIN01F

Table 2: Samples analyzed for comparison:

Description	Year	<i>n</i>	Life stage	Basin	Data source	Code
Big Beef Creek	2010	78	Returning adult	Hood Canal	ADFG	BBEEF10F
Big Beef Creek	2011	17	Returning adult	Hood Canal	ADFG	BBEEF11F
Big Mission Creek	2002	11	Returning adult	Hood Canal	UW	BIGM02F
Dewatto River	1998	63	Returning adult	Hood Canal	UW	DEW98F
Elwha River	2004	95	Returning adult	Strait of Juan de Fuca	ADFG	ELWH04F
Grays River	2000	48	Returning adult	Columbia River	UW	GRAY00F
Grays River	2001	47	Returning adult	Columbia River	UW	GRAY01F
Hamilton Creek	2004	95	Returning adult	Columbia River	ADFG	HAMIL04F
I-205 Seep	2000	84	Returning adult	Columbia River	UW	I205S00F
Skamokawa Creek	2002	72	Returning adult	Columbia River	UW	SKA02F
Satsop River	1998	95	Returning adult	Chehalis River	ADFG	SATS98F

Genetic markers analyzed:

Sixty-seven single nucleotide polymorphism (SNP) markers (Appendix 1).

Table 3: Diversity within samples

Expected (H_E) and observed (H_O) heterozygosity, number of loci exhibiting departures from Hardy-Weinberg Equilibrium (HWE), and F_{IS} (a measure of departure from random mating). Values of F_{IS} in bold were bounded by 95% confidence intervals that did not overlap zero.

Population	H_O	H_E	F_{IS}	HWE
QUIN01F	0.27	0.26	-0.0373	1
QUIN08F	0.27	0.25	-0.0658	2
QUIN10F	0.28	0.27	-0.0701	2
BBEEF10F	0.28	0.28	-0.0014	1
BBEEF11F	0.29	0.26	-0.1031	1
BIGM02F	0.25	0.23	-0.0595	0
DEW98F	0.28	0.26	-0.0630	2
ELWH04F	0.3	0.29	-0.0069	4
GRAY00F	0.26	0.25	-0.0490	1
GRAY01F	0.24	0.24	-0.0181	2
HAMIL04F	0.26	0.26	-0.0029	2
I205S00F	0.26	0.26	-0.0045	5
SKA02F	0.26	0.26	0.0069	5
SATS98F	NA	0.29	0.0966	2

Figure 1: Correspondence Analysis (CA) of allele frequencies observed in fall chum salmon from Quinault NFH and adjacent collection sites.

Sample numbers are those listed in Table 3. The primary (horizontal) axis accounted for 32.8% of the inertia in the data and the secondary (vertical) axis accounted for 19% of the inertia.

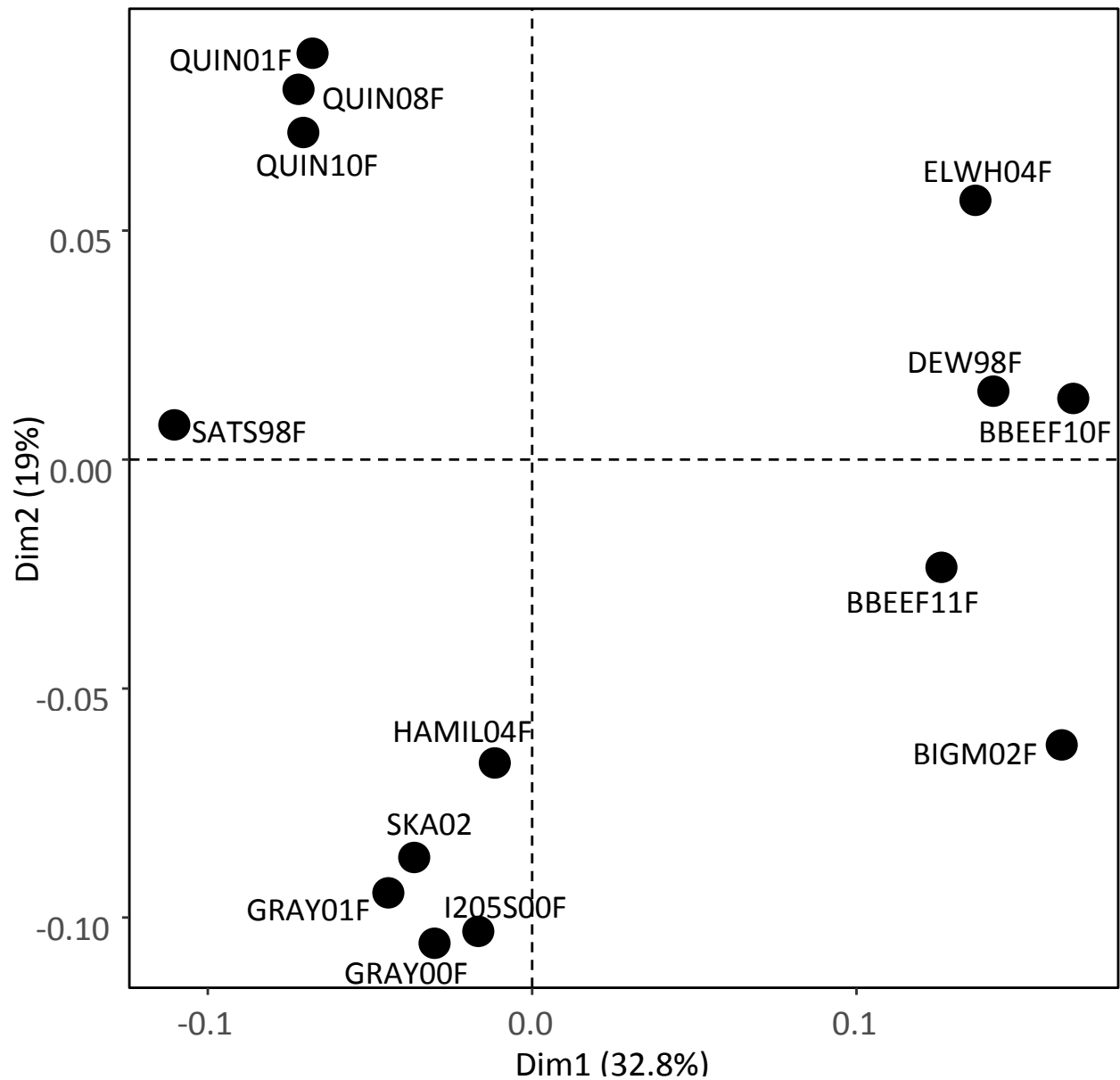


Figure 2: Estimates of effective population size (N_E) for fall chum salmon broodstock from Quinault NFH and adjacent collection sites.

N_E was estimated using the linkage-disequilibrium method. Each point estimate is surrounded by a jackknifed 95% confidence interval.

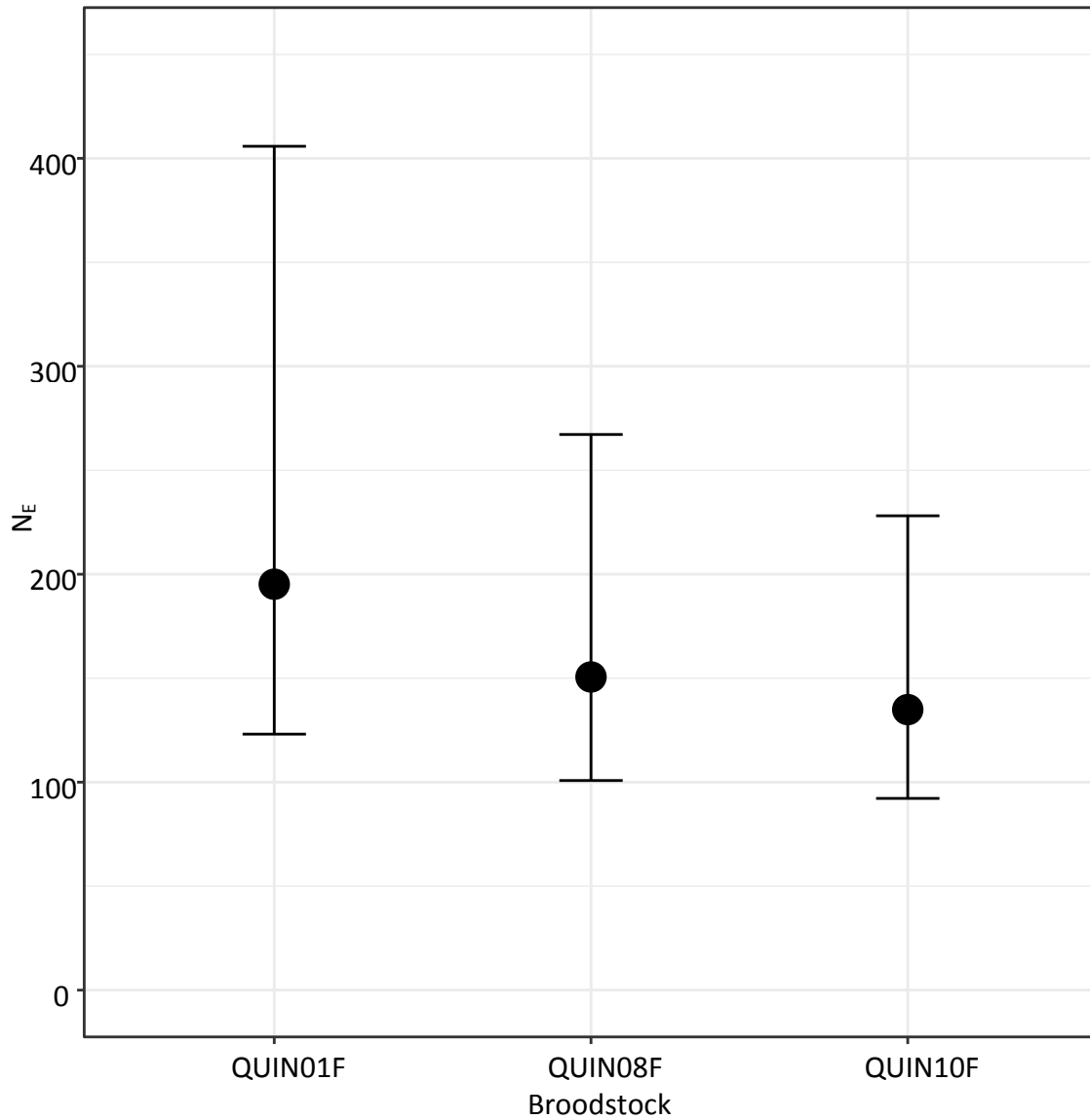
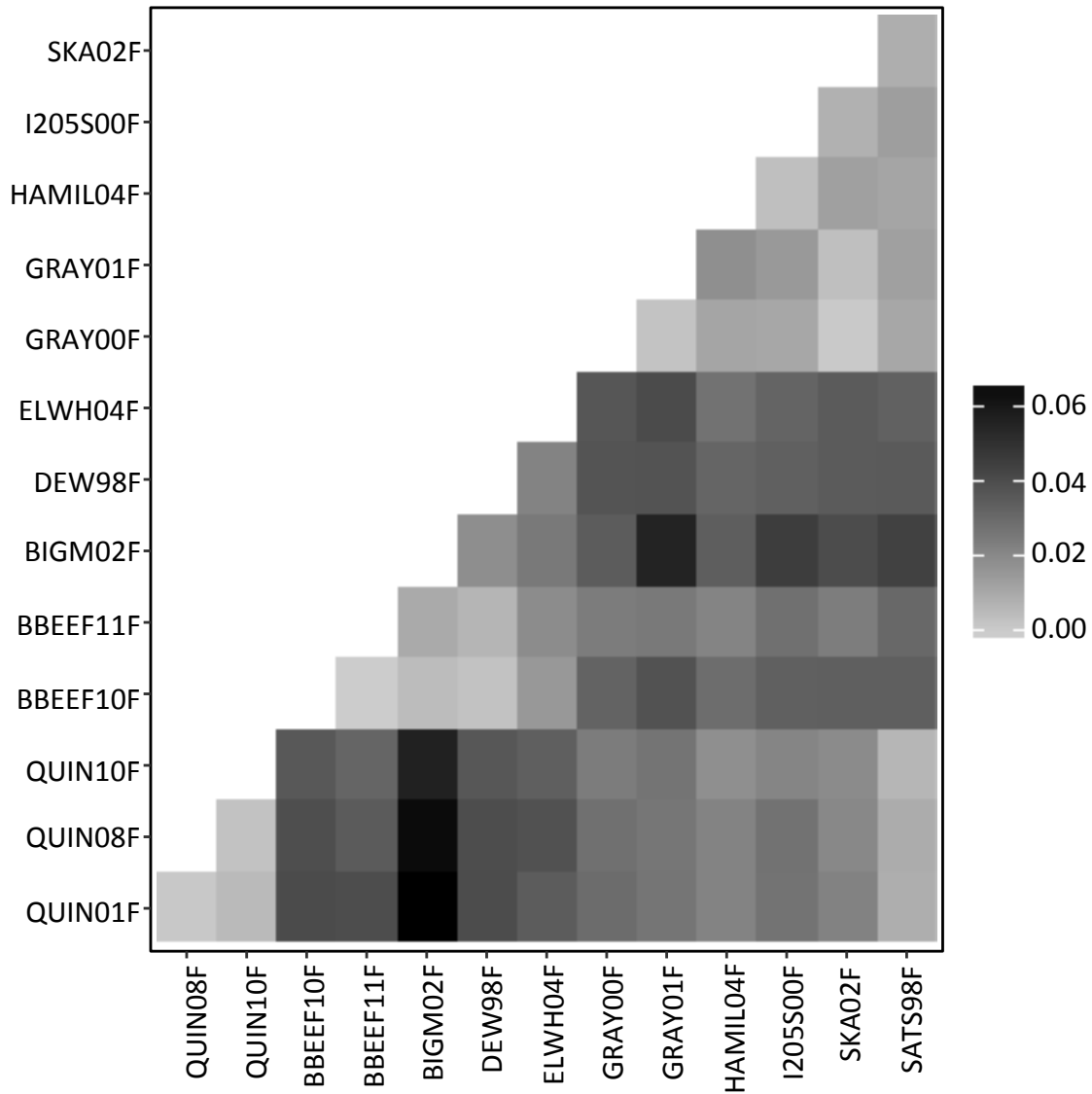


Figure 3: Heatmap of pairwise F_{ST} values between for fall chum broodstock from Quinault NFH and adjacent collection sites. Darker colors indicate greater genetic differentiation between populations.



Comments

- The goals of this report series are 1) to summarize available genetic information for NFH broodstocks and make that information available to hatchery managers, and 2) to make sure that data for the NFH broodstocks are available for internal hatchery reviews and HET meetings, as well as to our partners.
- Genetic diversity (heterozygosity) was similar across the various populations that were investigated. The tendency was for wild populations from Hood Canal and the Strait of Juan de Fuca to have higher diversity than those from the west coast of Washington. This corresponds to patterns observed for other wild populations (Beacham et al. 2009; Small et al. 2015)
- For the number of loci analyzed for this report (67), the number of loci deviating from HWE was low for these broodstocks (between 0-7%). All but two populations produced negative F_{IS} values, five of which were bounded by 95% confidence intervals that did not overlap zero. This included the three Quinault broodstocks. These results are indicative of an excess of heterozygotes compared to expectations under random mating. This pattern, negative F_{IS} with few HWE deviations, is unusual. Sampling additional years and recording additional data such as sex could elucidate potential mechanisms driving this pattern.
- Broodstock produced at Quinault NFH across multiple years clustered together in the CA plot, suggesting genetic similarity across cohorts. F_{ST} -values support this conclusion. Quinault broodstocks did not display strong associations with any other population and their position in the CA plot likely reflects the local origin of the broodstock. Wild populations from the Hood Canal and Columbia River formed the two main clusters. The population most similar genetically to Quinault chum was from Satsop Creek in the Chehalis River basin. Among this dataset the Satsop population was the closest in geographic proximity to the Quinault basin, also located on the west coast of Washington. This suggests the Quinault broodstock likely possesses no genetic ancestry derived from past out-of-basin egg transfers from the Hood Canal.
- Most of the F_{ST} comparisons produced confidence intervals that did not overlap zero (i.e. were statistically significant), which is one measure to judge the strength of differentiation. However, statistical power to detect differentiation can be affected sample

size, both in terms of number of loci and individuals. Both were relatively large for this analysis, which would have produced narrowed confidence intervals. The actual F_{ST} -values themselves, though, were low. This pattern of low but statistically significant differentiation has been observed in other studies of wild chum salmon populations in the Pacific Northwest (Small et al. 2006, 2009, 2015; Beacham et al. 2009). A metapopulation structure buoyed by historically large spawning aggregations with occasional gene flow due to straying likely generated this pattern.

- Estimates of effective population size at Quinault NFH showed a slight decline across the time period that was analyzed (from 195.2 in 2001 to 134.9 in 2010). However, confidence intervals overlapped between the estimates. Point estimates for Quinault were all below 200.

Availability

Genotype data for NFH stocks will be provided by AFTC upon request.

Disclaimer

The findings and conclusions in this report are those of the author and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

References

- BEACHAM, T., J. R. CANDY, K. D. LE AND M. WETKLO. 2009. Population structure of chum salmon (*Oncorhynchus keta*) across the Pacific Rim, determined from microsatellite analysis. *Fishery Bulletin* 107:244–260.
- SMALL, M. P. ET AL. 2015. Chum Salmon Genetic Diversity in the Northeastern Pacific Ocean Assessed with Single Nucleotide Polymorphisms (SNPs): Applications to Fishery Management. *North American Journal of Fisheries Management* 35:974–987.
- SMALL, M. P., K. CURRENS, T. H. JOHNSON, A. E. FRYE AND J. F. VON BARGEN. 2009. Impacts of supplementation: genetic diversity in supplemented and unsupplemented populations of summer chum salmon (*Oncorhynchus keta*) in Puget Sound (Washington, USA). *Canadian Journal of Fisheries and Aquatic Sciences* 66:1216–1229.
- SMALL, M. P., A. E. FRYE, J. F. VON BARGEN AND S. F. YOUNG. 2006. Genetic structure of chum salmon (*Oncorhynchus keta*) populations in the lower Columbia River: Are chum salmon in Cascade tributaries remnant populations? *Conservation Genetics* 7:65–78.

Appendix 1: Sixty-seven single nucleotide polymorphism (SNP) markers used to analyze Quinault NFH chum salmon.

SNPs	
Oke_ACOT-100	Oke_U2041-84
Oke_ras1-249	Oke_U2043-51
Oke_RFC2-618	Oke_U2048-91
Oke_RH1op-245	Oke_U2053-60
Oke_CKS1-94	Oke_U2056-90
Oke_RSPRY1-106	Oke_U2057-80
Oke_serpin-140	Oke_U212-87
Oke_slc1a3a-86	Oke_U302-195
Oke_sylc-90	Oke_DCXR-87
Oke_TCP1-78	Oke_U502-241
Oke_Tf-278	Oke_U504-228
Oke_CKS-389	Oke_U506-110
Oke_thic-84	Oke_U507-286
Oke_U1002-262	Oke_U509-219
Oke_U1008-83	Oke_eif4g1-43
Oke_U1010-251	Oke_FANK1-166
Oke_U1015-255	Oke_FBXL5-61
Oke_U1016-154	Oke_arf-319
Oke_U1017-52	Oke_GHII-3129
Oke_U1021-102	Oke_GPDH-191
Oke_U1022-139	Oke_GPH-105
Oke_U1023-147	Oke_HP-182
Oke_U1024-113	Oke_il-1racp-67
Oke_Cr30	Oke_KPNA2-87
Oke_u200-385	Oke_LAMP2-186
Oke_U2006-109	Oke_azin1-90
Oke_U2015-151	Oke_mgll-49
Oke_U2025-86	Oke_MLRN-63
Oke_U2029-79	Oke_nc2b-148
Oke_U2031-37	Oke_ND3-69
Oke_U2032-74	Oke_PPA2-635
Oke_U2034-55	Oke_rab5a-117
Oke_U2035-54	Oke_ccd16-77
Oke_U2037-76	

Appendix 2: Pairwise F_{ST} values between fall chum salmon broodstock produced at Quinault NFH and adjacent collection sites.

Bold values indicate comparisons for which the 95% confidence interval estimated using 1000 bootstrap replicates did not overlap zero. For SATS98F (in italics) confidence intervals could not be calculated.

	QUIN01F	QUIN08F	QUIN10F
BBEEF10F	0.0381	0.0373	0.0339
BBEEF11F	0.0374	0.033	0.0295
BIGM02F	0.0631	0.0608	0.0530
DEW98F	0.0378	0.0374	0.0343
ELWH04F	0.0326	0.036	0.0317
GRAY00F	0.0274	0.0262	0.0224
GRAY01F	0.0247	0.0244	0.0249
HAMIL04F	0.0201	0.0203	0.0166
I205S00F	0.0252	0.0256	0.0196
SATS98F	<i>0.0075</i>	<i>0.0081</i>	<i>0.0051</i>
SKA02F	0.0205	0.0188	0.0179
QUIN01F		-1.00E-04	0.0040
QUIN08F			0.0018
QUIN10F			

Appendix 3: Glossary

Allele – A unique genetic character state. Each locus has two alleles.

Effective population size (N_E) – The number of individuals in a model population which would lose genetic variation at the same rate as an observed population. Deviations from model behavior in real populations (e.g. unequal sex ratios, some individuals reproducing more than others, etc...) tend to make N_E lower than census size (N).

F_{IS} – Correlation of alleles in an individual relative to the subpopulation in which it occurs. Commonly used as a measure of departure from random mating within a subpopulation.

F_{ST} – Correlation of alleles within the same subpopulation relative to the entire population. Commonly used as a measure of divergence between subpopulations.

Gene flow – Movement of genetic material from one population to another. Implies both physical movement and successful integration into the recipient population.

Genetic Drift – Process of genetic divergence between populations based on random sampling of alleles each generation.

Heterozygosity – Proportion of individuals in a population that are heterozygotes (i.e. do not have two identical alleles at a locus).

Hardy-Weinberg Equilibrium (HWE) – Genotype ratios expected under a random mating model.

Locus – A physical location on the DNA of an organism. The term “locus” is often used synonymously with “marker” or with any type of marker (e.g., “SNP” or “microsatellite”).